

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/650,326B

Source: IFW0

Date Processed by STIC: 8/20/05

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IFWO

RAW SEQUENCE LISTING

DATE: 08/20/2005

PATENT APPLICATION: US/10/650,326B

TIME: 11:47:45

Input Set : A:\JJJ-P01-599.txt

Output Set: N:\CRF4\08202005\J650326B.raw

3 <110> APPLICANT: Hruska, Keith A.
 4 McCartney, John E.
 5 Charette, Marc F.
 7 <120> TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
 8 TREATMENT OF CHRONIC RENAL FAILURE
 10 <130> FILE REFERENCE: JJJ-P01-599
 12 <140> CURRENT APPLICATION NUMBER: 10/650,326B
 13 <141> CURRENT FILING DATE: 2003-08-28
 15 <150> PRIOR APPLICATION NUMBER: 60/406,431
 16 <151> PRIOR FILING DATE: 2002-08-28
 18 <160> NUMBER OF SEQ ID NOS: 31
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 139
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 30 1 5 10 15
 33 Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
 34 20 25 30
 37 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
 38 35 40 45
 41 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
 42 50 55 60
 45 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 46 65 70 75 80
 49 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 50 85 90 95
 53 Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 54 100 105 110
 57 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 58 115 120 125
 61 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 62 130 135
 65 <210> SEQ ID NO: 2
 66 <211> LENGTH: 97
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Homo sapiens
 70 <400> SEQUENCE: 2
 72 His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met Gln Arg Glu Ile
 73 1 5 10 15
 76 Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly

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```

77          20          25          30
80 Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met
81          35          40          45
84 Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro
85          50          55          60
88 Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln
89 65          70          75          80
92 Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn
93          85          90          95
96 Leu
99 <210> SEQ ID NO: 3
100 <211> LENGTH: 431
101 <212> TYPE: PRT
102 <213> ORGANISM: Homo sapiens
104 <400> SEQUENCE: 3
106 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
107 1          5          10          15
110 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
111          20          25          30
114 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
115          35          40          45
118 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
119          50          55          60
122 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
123 65          70          75          80
126 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
127          85          90          95
130 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
131          100          105          110
134 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
135          115          120          125
138 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
139          130          135          140
142 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
143 145          150          155          160
146 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
147          165          170          175
150 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
151          180          185          190
154 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
155          195          200          205
158 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
159          210          215          220
162 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
163 225          230          235          240
166 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
167          245          250          255
170 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
171          260          265          270

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174 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
175          275          280          285
178 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
179          290          295          300
182 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
183 305          310          315          320
186 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
187          325          330          335
190 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
191          340          345          350
194 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
195          355          360          365
198 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
199          370          375          380
202 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
203 385          390          395          400
206 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
207          405          410          415
210 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
211          420          425          430
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 139
216 <212> TYPE: PRT
217 <213> ORGANISM: Mus musculus
219 <400> SEQUENCE: 4
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222 1          5          10          15
225 Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser
226          20          25          30
229 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
230          35          40          45
233 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
234          50          55          60
237 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
238 65          70          75          80
241 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
242          85          90          95
245 Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
246          100          105          110
249 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
250          115          120          125
253 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
254          130          135
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 139
259 <212> TYPE: PRT
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 5
264 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu

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```

265 1          5          10          15
268 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser
269          20          25          30
272 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
273          35          40          45
276 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
277          50          55          60
280 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
281 65          70          75          80
284 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
285          85          90          95
288 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
289          100          105          110
292 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
293          115          120          125
296 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
297          130          135
300 <210> SEQ ID NO: 6
301 <211> LENGTH: 139
302 <212> TYPE: PRT
303 <213> ORGANISM: Mus musculus
305 <400> SEQUENCE: 6
307 Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu
308 1          5          10          15
311 Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
312          20          25          30
315 Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg
316          35          40          45
319 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
320          50          55          60
323 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn
324 65          70          75          80
327 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
328          85          90          95
331 Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
332          100          105          110
335 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
336          115          120          125
339 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
340          130          135
343 <210> SEQ ID NO: 7
344 <211> LENGTH: 588
345 <212> TYPE: PRT
346 <213> ORGANISM: Drosophila melanogaster
348 <400> SEQUENCE: 7
350 Met Arg Ala Trp Leu Leu Leu Leu Ala Val Leu Ala Thr Phe Gln Thr
351 1          5          10          15
354 Ile Val Arg Val Ala Ser Thr Glu Asp Ile Ser Gln Arg Phe Ile Ala
355          20          25          30

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```

358 Ala Ile Ala Pro Val Ala Ala His Ile Pro Leu Ala Ser Ala Ser Gly
359          35          40          45
362 Ser Gly Ser Gly Arg Ser Gly Ser Arg Ser Gly Gly Ala Ser Thr Ser
363          50          55          60
366 Thr Ala Leu Ala Lys Ala Phe Asn Pro Phe Ser Glu Pro Ala Ser Phe
367 65          70          75          80
370 Ser Asp Ser Asp Lys Ser His Arg Ser Lys Thr Asn Lys Lys Pro Ser
371          85          90          95
374 Lys Ser Asp Ala Asn Arg Gln Phe Asn Glu Val His Lys Pro Arg Thr
375          100          105          110
378 Asp Gln Leu Glu Asn Ser Lys Asn Met Ser Lys Gln Leu Val Asn Lys
379          115          120          125
382 Pro Asn His Asn Lys Met Ala Val Lys Glu Gln Arg Ser His His Lys
383          130          135          140
386 Lys Ser His His His Arg Ser His Gln Pro Lys Gln Ala Ser Ala Ser
387 145          150          155          160
390 Thr Glu Ser His Gln Ser Ser Ser Ile Glu Ser Ile Phe Val Glu Glu
391          165          170          175
394 Pro Thr Leu Val Leu Asp Arg Glu Val Ala Ser Ile Asn Val Pro Ala
395          180          185          190
398 Asn Ala Lys Ala Ile Ile Ala Glu Gln Gly Pro Ser Thr Tyr Ser Lys
399          195          200          205
402 Glu Ala Leu Ile Lys Asp Lys Leu Lys Pro Asp Pro Ser Thr Leu Val
403          210          215          220
406 Glu Ile Glu Lys Ser Leu Leu Ser Leu Phe Asn Met Lys Arg Pro Pro
407 225          230          235          240
410 Lys Ile Asp Arg Ser Lys Ile Ile Ile Pro Glu Pro Met Lys Lys Leu
411          245          250          255
414 Tyr Ala Glu Ile Met Gly His Glu Leu Asp Ser Val Asn Ile Pro Lys
415          260          265          270
418 Pro Gly Leu Leu Thr Lys Ser Ala Asn Thr Val Arg Ser Phe Thr His
419          275          280          285
422 Lys Asp Ser Lys Ile Asp Asp Arg Phe Pro His His His Arg Phe Arg
423          290          295          300
426 Leu His Phe Asp Val Lys Ser Ile Pro Ala Asp Glu Lys Leu Lys Ala
427 305          310          315          320
430 Ala Glu Leu Gln Leu Thr Arg Asp Ala Leu Ser Gln Gln Val Val Ala
431          325          330          335
434 Ser Arg Ser Ser Ala Asn Arg Thr Arg Tyr Gln Val Leu Val Tyr Asp
435          340          345          350
438 Ile Thr Arg Val Gly Val Arg Gly Gln Arg Glu Pro Ser Tyr Leu Leu
439          355          360          365
442 Leu Asp Thr Lys Thr Val Arg Leu Asn Ser Thr Asp Thr Val Ser Leu
443          370          375          380
446 Asp Val Gln Pro Ala Val Asp Arg Trp Leu Ala Ser Pro Gln Arg Asn
447 385          390          395          400
450 Tyr Gly Leu Leu Val Glu Val Arg Thr Val Arg Ser Leu Lys Pro Ala
451          405          410          415
454 Pro His His His Val Arg Leu Arg Arg Ser Ala Asp Glu Ala His Glu

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/650,326B

DATE: 08/20/2005
TIME: 11:47:46

Input Set : A:\JJJ-P01-599.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; Xaa Pos. 2,3,4,6,7,8,11,12,13,14,15,16,18,19,20,21,23,26,28,30,31
 Seq#:24; Xaa Pos. 33,34,35,36,37,38,39,40,44,45,46,47,48,49,50,51,52,53,54
 Seq#:24; Xaa Pos. 55,56,57,58,59,60,63,65,66,67,68,69,70,71,72,74,75,76,77
 Seq#:24; Xaa Pos. 78,79,80,82,84,85,86,87,88,90,92,93,95,97
 Seq#:25; Xaa Pos. 2,3,4,5,7,8,9,11,12,13,16,17,18,19,20,21,23,24,25,26,28
 Seq#:25; Xaa Pos. 31,33,35,36,38,39,40,41,42,43,44,45,49,50,51,52,53,54,55
 Seq#:25; Xaa Pos. 56,57,58,59,60,61,62,63,64,65,68,70,71,72,73,74,75,76,77
 Seq#:25; Xaa Pos. 79,80,81,82,83,84,85,87,89,90,91,92,93,95,97,98,100,102
 Seq#:26; Xaa Pos. 2,3,4,5
 Seq#:27; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23
 Seq#:27; Xaa Pos. 24,26,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
 Seq#:27; Xaa Pos. 46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,63,65,66
 Seq#:27; Xaa Pos. 67,68,69,70,71,72,74,75,76,77,78,79,80,81,82,83,84,85,86
 Seq#:27; Xaa Pos. 87,88,89,90,91,92,93,95,97
 Seq#:28; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,23,24
 Seq#:28; Xaa Pos. 25,26,27,28,29,31,33,35,36,37,38,39,40,41,42,43,44,45,46
 Seq#:28; Xaa Pos. 47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
 Seq#:28; Xaa Pos. 66,68,70,71,72,73,74,75,76,77,79,80,81,82,83,84,85,86,87
 Seq#:28; Xaa Pos. 88,89,90,91,92,93,94,95,96,97,98,100,102
 Seq#:29; Xaa Pos. 2,3,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
 Seq#:29; Xaa Pos. 75,80,82,84,89,96
 Seq#:30; Xaa Pos. 2,3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:24; Line(s) 2080
 Seq#:25; Line(s) 2484
 Seq#:26; Line(s) 2890
 Seq#:27; Line(s) 2924
 Seq#:28; Line(s) 3403
 Seq#:29; Line(s) 3893

VERIFICATION SUMMARY

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Input Set : A:\JJJ-P01-599.txt

Output Set: N:\CRF4\08202005\J650326B.raw

L:2451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24
L:2856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:2914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:3369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:3405 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3507 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3741 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3749 M:283 W: Missing Blank Line separator, <220> field identifier
L:3857 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:4039 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:4041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29
L:4083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0